

AMENDMENTS TO CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for predicting the interaction between proteins based on a domain combination pair, comprising the steps of:

(a) selecting a domain combination pair from an interacting set of protein pairs and a non-interacting set of protein pairs;

(b) obtaining and storing information concerning a frequency of appearance frequency information of a designated the selected domain combination pair selected from each of interacting and non-interacting sets of protein pairs, and storing the obtained appearance frequency information (hereinafter, appearance frequency information);

(b) ©) determining defining a probability equation applied to predict that predicts the interaction between two proteins of the selected domain combination pair using the stored appearance frequency information of the domain combination; and

©) (d) obtaining an interaction probability value between the two proteins from the determined probability equation,

wherein the step ©) includes the sub-steps of:

determining a function which maps the selected domain combination pair to a real number in a designated range;

generating and storing a prediction distribution having values obtained by applying the determined function to a protein pair which configures the interacting and non-interacting sets of protein pairs; and

defining the probability equation that predicts the interaction between two proteins using the stored prediction distributions.

2. (Original) The prediction method as set forth in claim 1, wherein the step (a) includes the sub-steps of:

- (a-1) creating a weighted appearance frequency; and
- (a-2) creating an appearance probability (AP) matrix based on the weighted appearance frequency.

3. (Currently Amended) The prediction method as set forth in claim 1, wherein:

the appearance frequency information of the domain combination is defined by an appearance probability (AP) matrix; and

an element AP_{ij} of the AP matrix is determined by below Equations,

$$AP_{ij} = \frac{WF_{ij}}{\sum_{i,j} WF_{ij}}$$

$$WF_{ab} = \sum_{\substack{\text{For all protein pairs } p_i, q_j \\ \text{s.t. } \langle a, b \rangle \in dc\text{-pair}(p_i, q_j)}} \frac{1}{|dc(p_i)| \times |dc(q_j)|}$$

where WF_{ab} is a weighted appearance frequency of domain combination $\langle a, b \rangle$, $dc(p)$ is the set of all possible domain combinations of protein p , and $dc(q)$ is the set of all possible domain combinations of protein q .

4. (Currently Amended) The prediction method as set forth in claim 1, wherein the step (c) (d) includes the sub-steps of:

(c-1) (d-1) obtaining probability values and distributions of the probability values by applying the determined probability equation to the interacting and non-interacting sets of protein pairs;

(c-2)-(d-2) obtaining a probability value by applying the determined probability equation to the given protein pair; and

(c-3)-(d-3) computing a probability for determining which set the given protein pair belongs to based on the distributions of the interacting and non-interacting sets of protein pairs.

5. (Canceled)

6. (Canceled)

7. (Canceled)